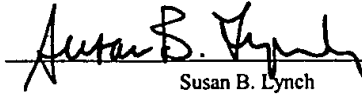


CERTIFICATE OF MAILING BY "FIRST CLASS MAIL"

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to:
USPTO, Box Sequence, PO Box 2327, Arlington, VA 22202, on March 28, 2002.


Susan B. Lynch

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Daniel E. AFAR et al.

Serial No.: 10/010,667

Filing Date: 06 December 2001

For: PEPTIDES DERIVED FROM STEAP1
(AS AMENDED)



Examiner: To be assigned

Group Art Unit: To be assigned

RESPONSE TO NOTICE TO FILE CORRECTED APPLICATION PAPERS

Box Sequence
Assistant Commissioner for Patents
P.O. Box 2327
Arlington, VA 22202

Dear Sir:

This is in response to the Notice to file Corrected Application Papers of nonprovisional application 10/010,667 mailed January 29, 2002, for which a response is due on March 29, 2002. Accordingly, this response is timely filed.

Please enter the following Sequence Listing, amendments and remarks.



In the Sequence Listing:

Please insert the attached paper copy of the Sequence Listing as new pages 1-10 in the above-captioned application. A computer-readable form copy (CRF copy) of the Sequence Listing accompanies this response.

AMENDMENTS

In the Specification

Please replace the paragraph beginning at page 5, line 35, with the following rewritten paragraph:

FIG. 4-1- 4-2. Nucleotide sequence of STEAP-1 GTH9 clone (SEQ ID NO:6) corresponding to the 4 kb message on northern blots (FIG. 3A). The sequence contains an intron of 2399 base pairs relative to the STEAP-1 clone 10 sequence of FIG. 1A; coding regions are nucleotides 96-857 and 3257-3510 (indicated in bold). The start ATG is in bold and underlined, the STOP codon is in bold and underlined, and the intron-exon boundaries are underlined.--

Please replace the paragraph beginning at page 7, line 23, with the following rewritten paragraph:

-- FIG. 11. Primary structural comparison of STEAP family proteins. FIG. 11A. Amino acid sequence alignment of STEAP-1 (8P1D4 CLONE 10; SEQ ID NO:2) and STEAP-2 (98P4B6;SEQ ID NO: 8) sequences. The alignment was performed using the SIM alignment program of the Baylor College of Medicine Search Launcher Web site. Results show a 61.4% identity in a 171 amino acid overlap; Score: 576.0; Gap frequency: 0.0%. FIG. 11B. Amino acid sequence alignment of STEAP-1 with partial ORF sequences of STEAP-2 and two other putative family member proteins using PIMA program (PIMA 1.4 program at Internet address <<http://dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align.html>>); transmembrane domains identified by the SOSUI program (available at Internet address <http://www.tuat.ac.jp/~mitaku/adv_sosui/submit.html>). are in bold.--